



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: SHEEN, JEN
- (ii) TITLE OF THE INVENTION: STRESS PROTECTED TRANSGENIC PLANTS
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Clark & Elbing LLP
  - (B) STREET: 176 Federal Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/989,881
  - (B) FILING DATE: 12-DEC-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 60/032,966
  - (B) FILING DATE: 13-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Elbing, Karen L
  - (B) REGISTRATION NUMBER: 35,238
  - (C) REFERENCE/DOCKET NUMBER: 08472/716002
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 617-428-0200
  - (B) TELEFAX: 617-428-7045
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1020 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 97...918
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTGTAAAC			GACGGNCAGT			GAATTGTAAT			ACGACTCNCT			ATAGGGCGNA			ATTGGAGCTC			60
CACCGCGGTG			GCGGCCGCTC			TAGAACTAGT			GGATCC			ATG	GCT	AAT	CAA	ACT	CAG	114
												Met	Ala	Asn	Gln	Thr	Gln	
												1				5		
ATC	AGC	GAC	AAG	TAC	ATC	TTA	GGA	CGA	GAA	CTC	GGT	CGC	GGC	GAA	TTC		162	
Ile	Ser	Asp	Lys	Tyr	Ile	Leu	Gly	Arg	Glu	Leu	Gly	Arg	Gly	Glu	Phe			
			10						15			20						
GGA	ATC	ACG	TAT	CTT	TGT	ACA	GAT	AGA	GAG	ACT	CGT	GAA	GCT	TTA	GCT		210	
Gly	Ile	Thr	Tyr	Leu	Cys	Thr	Asp	Arg	Glu	Thr	Arg	Glu	Ala	Leu	Ala			
			25			30			35									
TGC	AAA	TCA	ATC	TCC	AAG	AGA	AAG	CTC	CGA	ACC	GCC	GTC	GAT	GTG	GAA		258	
Cys	Lys	Ser	Ile	Ser	Lys	Arg	Lys	Leu	Arg	Thr	Ala	Val	Asp	Val	Glu			
			40			45			50									
GAC	GTC	CGT	CGT	GAA	GTC	ACG	ATC	ATG	TCA	ACT	TTA	CCG	GAA	CAC	CCA		306	
Asp	Val	Arg	Arg	Glu	Val	Thr	Ile	Met	Ser	Thr	Leu	Pro	Glu	His	Pro			
			60			65			70									
AAC	GTT	GTG	AAA	CTT	AAA	GCG	ACT	TAT	GAG	GAT	AAC	GAG	ACC	GTG	CAT		354	
Asn	Val	Val	Lys	Leu	Lys	Ala	Thr	Tyr	Glu	Asp	Asn	Glu	Thr	Val	His			
			75			80			85									
CTT	GTG	ATG	GAG	CTT	TGT	GAA	GGA	GGT	GAG	CTT	TTT	GGT	CGG	ATT	GTT		402	
Leu	Val	Met	Glu	Leu	Cys	Glu	Gly	Gly	Glu	Leu	Phe	Gly	Arg	Ile	Val			
			90			95			100									
GCA	AGA	GGA	CAT	TAT	ACA	GAG	CGT	GCG	GCG	GCT	ACC	GTC	GCG	AGA	ACG		450	
Ala	Arg	Gly	His	Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Thr	Val	Ala	Arg	Thr			
			105			110			115									
ATC	GCG	GAA	GTT	GTG	AGG	ATG	TGT	CAT	GTC	AAT	GGT	GTT	ATG	CAT	AGA		498	
Ile	Ala	Glu	Val	Val	Arg	Met	Cys	His	Val	Asn	Gly	Val	Met	His	Arg			
			120			125			130									
GAT	TTG	AAG	CCT	GAG	AAT	TTC	TTG	TTT	GCT	AAC	AAG	AAG	GAG	AAT	TCT		546	
Asp	Leu	Lys	Pro	Glu	Asn	Phe	Leu	Phe	Ala	Asn	Lys	Lys	Glu	Asn	Ser			
			135			140			145						150			
GCA	CTT	AAG	GCT	ATT	GAT	TTT	GGT	TTA	TCT	GTT	CTC	TTT	AAA	CCT	GGA		594	
Ala	Leu	Lys	Ala	Ile	Asp	Phe	Gly	Leu	Ser	Val	Leu	Phe	Lys	Pro	Gly			
			155			160			165									
GAG	AGG	TTT	ACA	GAG	ATT	GTT	GGA	AGT	CCT	TAT	TAT	ATG	GCT	CCA	GAA		642	
Glu	Arg	Phe	Thr	Glu	Ile	Val	Gly	Ser	Pro	Tyr	Tyr	Met	Ala	Pro	Glu			
			170			175			180									
GTG	TTG	AAG	AGA	AAT	TAT	GGA	CCA	GAG	GTT	GAT	GTG	TGG	AGT	GCT	GGA		690	
Val	Leu	Lys	Arg	Asn	Tyr	Gly	Pro	Glu	Val	Asp	Val	Trp	Ser	Ala	Gly			
			185			190			195									
GTT	ATC	CTC	TAC	ATC	TTG	CTT	TGT	GGT	GTT	CCT	CCG	TTT	TGG	GCA	GAG		738	
Val	Ile	Leu	Tyr	Ile	Leu	Leu	Cys	Gly	Val	Pro	Pro	Phe	Trp	Ala	Glu			
			200			205			210									
ACT	GAA	CAA	GGT	GTG	GCT	CTT												





SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: SHEEN, JEN
- (ii) TITLE OF THE INVENTION: STRESS PROTECTED TRANSGENIC PLANTS
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Clark & Elbing LLP
  - (B) STREET: 176 Federal Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/989,881
  - (B) FILING DATE: 12-DEC-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 60/032,966
  - (B) FILING DATE: 13-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Elbing, Karen L
  - (B) REGISTRATION NUMBER: 35,238
  - (C) REFERENCE/DOCKET NUMBER: 08472/716002
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 617-428-0200
  - (B) TELEFAX: 617-428-7045
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 97...918
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTGTAAAC GACGGNCAGT GAATTGTAAT ACGACTCNCT ATAGGGCGNA ATTGGAGCTC 60  
CACCGCGGTG GCGGCCGCTC TAGAACTAGT GGATCC ATG GCT AAT CAA ACT CAG 114  
Met Ala Asn Gln Thr Gln  
1 5

ATC AGC GAC AAG TAC ATC TTA GGA CGA GAA CTC GGT CGC GGC GAA TTC 162  
Ile Ser Asp Lys Tyr Ile Leu Gly Arg Glu Leu Gly Arg Gly Glu Phe  
10 15 20

GGA ATC ACG TAT CTT TGT ACA GAT AGA GAG ACT CGT GAA GCT TTA GCT 210  
Gly Ile Thr Tyr Leu Cys Thr Asp Arg Glu Thr Arg Glu Ala Leu Ala  
25 30 35

TGC AAA TCA ATC TCC AAG AGA AAG CTC CGA ACC GCC GTC GAT GTG GAA 258  
Cys Lys Ser Ile Ser Lys Arg Lys Leu Arg Thr Ala Val Asp Val Glu  
40 45 50

GAC GTC CGT CGT GAA GTC ACG ATC ATG TCA ACT TTA CCG GAA CAC CCA 306  
Asp Val Arg Arg Glu Val Thr Ile Met Ser Thr Leu Pro Glu His Pro  
55 60 65 70

AAC GTT GTG AAA CTT AAA GCG ACT TAT GAG GAT AAC GAG ACC GTG CAT 354  
Asn Val Val Lys Leu Lys Ala Thr Tyr Glu Asp Asn Glu Thr Val His  
75 80 85

CTT GTG ATG GAG CTT TGT GAA GGA GGT GAG CTT TTT GGT CGG ATT GTT 402  
Leu Val Met Glu Leu Cys Glu Gly Gly Glu Leu Phe Gly Arg Ile Val  
90 95 100

GCA AGA GGA CAT TAT ACA GAG CGT GCG GCG GCT ACC GTC GCG AGA ACG 450  
Ala Arg Gly His Tyr Thr Glu Arg Ala Ala Ala Thr Val Ala Arg Thr  
105 110 115

ATC GCG GAA GTT GTG AGG ATG TGT CAT GTC AAT GGT GTT ATG CAT AGA 498  
Ile Ala Glu Val Val Arg Met Cys His Val Asn Gly Val Met His Arg

120	125	130	
GAT TTG AAG CCT GAG AAT TTC TTG TTT GCT AAC AAG AAG GAG AAT TCT			546
Asp Leu Lys Pro Glu Asn Phe Leu Phe Ala Asn Lys Lys Glu Asn Ser			
135	140	145	150
GCA CTT AAG GCT ATT GAT TTT GGT TTA TCT GTT CTC TTT AAA CCT GGA			594
Ala Leu Lys Ala Ile Asp Phe Gly Leu Ser Val Leu Phe Lys Pro Gly			
	155	160	165
GAG AGG TTT ACA GAG ATT GTT GGA AGT CCT TAT TAT ATG GCT CCA GAA			642
Glu Arg Phe Thr Glu Ile Val Gly Ser Pro Tyr Tyr Met Ala Pro Glu			
	170	175	180
GTG TTG AAG AGA AAT TAT GGA CCA GAG GTT GAT GTG TGG AGT GCT GGA			690
Val Leu Lys Arg Asn Tyr Gly Pro Glu Val Asp Val Trp Ser Ala Gly			
	185	190	195
GTT ATC CTC TAC ATC TTG CTT TGT GGT GTT CCT CCG TTT TGG GCA GAG			738
Val Ile Leu Tyr Ile Leu Leu Cys Gly Val Pro Pro Phe Trp Ala Glu			
	200	205	210
ACT GAA CAA GGT GTG GCT CTT GCC ATC TTG AGG GGA GTT CTT GAT TTT			786
Thr Glu Gln Gly Val Ala Leu Ala Ile Leu Arg Gly Val Leu Asp Phe			
	215	220	225
AAG AGA GAT CCT TGG TCG CAG ATA TCA GAG AGC GCA AAG AGC CTT GTG			834
Lys Arg Asp Pro Trp Ser Gln Ile Ser Glu Ser Ala Lys Ser Leu Val			
	235	240	245
AAG CAG ATG TTG GAA CCT GAT TCA ACT AAG CGT TTG ACT GCT CAG CAA			882
Lys Gln Met Leu Glu Pro Asp Ser Thr Lys Arg Leu Thr Ala Gln Gln			
	250	255	260
GTT CTT GAT CAC CCT TGG ATA CAG AAT GCA AAG AAA AGGATCAAGC TTATCG			934
Val Leu Asp His Pro Trp Ile Gln Asn Ala Lys Lys			
	265	270	
ATACCGTCGA CCTCGAGGGG GGGCCCGGTA CCAGCTTTNG TTCCCTTTAG TGAGGGTTAA			994
TTTCGAGCTT GGC GTAATCA TGTCAT			1020

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asn Gln Thr Gln Ile Ser Asp Lys Tyr Ile Leu Gly Arg Glu  
1 5 10 15  
Leu Gly Arg Gly Glu Phe Gly Ile Thr Tyr Leu Cys Thr Asp Arg Glu  
20 25 30  
Thr Arg Glu Ala Leu Ala Cys Lys Ser Ile Ser Lys Arg Lys Leu Arg  
35 40 45  
Thr Ala Val Asp Val Glu Asp Val Arg Arg Glu Val Thr Ile Met Ser  
50 55 60  
Thr Leu Pro Glu His Pro Asn Val Val Lys Leu Lys Ala Thr Tyr Glu  
65 70 75 80  
Asp Asn Glu Thr Val His Leu Val Met Glu Leu Cys Glu Gly Gly Glu  
85 90 95  
Leu Phe Gly Arg Ile Val Ala Arg Gly His Tyr Thr Glu Arg Ala Ala  
100 105 110  
Ala Thr Val Ala Arg Thr Ile Ala Glu Val Val Arg Met Cys His Val  
115 120 125  
Asn Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu Phe Ala  
130 135 140  
Asn Lys Lys Glu Asn Ser Ala Leu Lys Ala Ile Asp Phe Gly Leu Ser  
145 150 155 160  
Val Leu Phe Lys Pro Gly Glu Arg Phe Thr Glu Ile Val Gly Ser Pro  
165 170 175  
Tyr Tyr Met Ala Pro Glu Val Leu Lys Arg Asn Tyr Gly Pro Glu Val  
180 185 190  
Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Cys Gly Val  
195 200 205  
Pro Pro Phe Trp Ala Glu Thr Glu Gln Gly Val Ala Leu Ala Ile Leu  
210 215 220  
Arg Gly Val Leu Asp Phe Lys Arg Asp Pro Trp Ser Gln Ile Ser Glu  
225 230 235 240  
Ser Ala Lys Ser Leu Val Lys Gln Met Leu Glu Pro Asp Ser Thr Lys  
245 250 255  
Arg Leu Thr Ala Gln Gln Val Leu Asp His Pro Trp Ile Gln Asn Ala  
260 265 270  
Lys Lys